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RAW SEQUENCE LISTING

DATE: 01/28/2002

PATENT APPLICATION: US/09/991,119

TIME: 16:40:57

Input Set : N:\Crf3\RULE60\09991119.raw

Output Set: N:\CRF3\01282002\I991119.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: LIN, LEU-FEN

6 COLLINS, FRANKLIN D.

7 DOHERTY, DANIEL H.

8 LILE, JACK

9 BEKTESH, SUSAN

11 (ii) TITLE OF INVENTION: Glial Cell Line-Derived Neurotrophic Factor

12 (iii) NUMBER OF SEQUENCES: 25

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: AMGEN INC.

15 (B) STREET: 1840 DeHavilland Drive

16 (C) CITY: Thousand Oaks

17 (D) STATE: California

18 (E) COUNTRY: USA

19 (F) ZIP: 91320-1789

20 (v) COMPUTER READABLE FORM:

21 (A) MEDIUM TYPE: Floppy Disk

22 (B) COMPUTER: Macintosh

23 (C) OPERATING SYSTEM: 7.1

24 (D) SOFTWARE: Microsoft Word 5.1

27 (vi) CURRENT APPLICATION DATA:

C--> 28 (A) APPLICATION NUMBER: US/09/991,119

C--> 29 (B) FILING DATE: 13-Nov-2001

32 (vii) PRIOR APPLICATION DATA:

33 (A) APPLICATION NUMBER: 08/452,229

34 (B) FILING DATE:

37 (2) INFORMATION FOR SEQ ID NO: 1:

38 (i) SEQUENCE CHARACTERISTICS:

39 (A) LENGTH: 25 amino acids

40 (B) TYPE: amino acid

41 (D) TOPOLOGY: linear

42 (v) FRAGMENT TYPE: N-terminal fragment

44 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

W--> 46 Ser Pro Asp Lys Gln Ala Ala Ala Leu Pro Arg Arg Glu Arg Asn Xaa

47 5 10 15

49 Gln Ala Ala Ala Ala Ser Pro Asp Asn

50 20 25

52 (2) INFORMATION FOR SEQ ID NO: 2:

53 (i) SEQUENCE CHARACTERISTICS:

54 (A) LENGTH: 13 amino acids

55 (B) TYPE: amino acid

C--> 56 (D) TOPOLOGY: linear

ENTERED

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57      (v) FRAGMENT TYPE: internal fragment
W--> 58      OTHER INFORMATION: Xaa is either Lys or Gln
60      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
W--> 63 Asp Xaa Ile Leu Lys Asn Leu Gly Arg Val Arg Arg Leu
64          5              10
66 (2) INFORMATION FOR SEQ ID NO: 3:
67      (i) SEQUENCE CHARACTERISTICS:
68          (A) LENGTH: 900 base pairs
69          (B) TYPE: nucleic acid
70          (C) STRANDEDNESS: single
71          (D) TOPOLOGY: linear
72      (ix) FEATURE:
73          (A) NAME/KEY: nucleic acid for rat GDNF
75      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
77 CCCCCGGGCT GCAGGAATTC GGGG GTC TAC GGA GAC CGG ATC CGA GGT      48
78          Val Tyr Gly Asp Arg Ile Arg Gly
79          -90
81 GCC GCC GCC GGA CGG GAC TCT AAG ATG AAG TTA TGG GAT GTC GTG      93
82 Ala Ala Ala Gly Arg Asp Ser Lys Met Lys Leu Trp Asp Val Val
83 -85          -80          -75
85 GCT GTC TGC CTG GTG TTG CTG CAC ACC GCG TCT GCC TTC CCG CTG      138
86 Ala Val Cys Leu Val Leu Leu His Thr Ala Ser Ala Phe Pro Leu
87 -70          -65          -60
89 CCC GCC GGT AAG AGG CTT CTC GAA GCG CCC GCC GAA GAC CAC TCC      183
90 Pro Ala Gly Lys Arg Leu Leu Glu Ala Pro Ala Glu Asp His Ser
91 -55          -50          -45
93 CTC GGC CAC CGC CGC GTG CCC TTC GCG CTG ACC AGT GAC TCC AAT      228
94 Leu Gly His Arg Arg Val Pro Phe Ala Leu Thr Ser Asp Ser Asn
95 -40          -35          -30
97 ATG CCC GAA GAT TAT CCT GAC CAG TTT GAT GAC GTC ATG GAT TTT      273
98 Met Pro Glu Asp Tyr Pro Asp Gln Phe Asp Asp Val Met Asp Phe
99 -25          -20          -15
101 ATT CAA GCC ACC ATC AAA AGA CTG AAA AGG TCA CCA GAT AAA CAA      318
102 Ile Gln Ala Thr Ile Lys Arg Leu Lys Arg Ser Pro Asp Lys Gln
103 -10          -5              1              5
105 GCG GCG GCA CTT CCT CGA AGA GAG AGG AAC CGG CAA GCT GCA GCT      363
106 Ala Ala Ala Leu Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala Ala
107          10              15              20
109 GCC AGC CCA GAG AAT TCC AGA GGG AAA GGT CGC AGA GGC CAG AGG      408
110 Ala Ser Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg
111          25              30              35
114 GGC AAA AAT CGG GGG TGC GTC TTA ACT GCA ATA CAC TTA AAT GTC      453
115 Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu Asn Val
116          40              45              50
118 ACT GAC TTG GGT TTG GGC TAC GAA ACC AAG GAG GAA CTG ATC TTT      498
119 Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe
120          55              60              65
122 CGA TAT TGT AGC GGT TCC TGT GAA GCG GCC GAG ACA ATG TAC GAC      543
123 Arg Tyr Cys Ser Gly Ser Cys Glu Ala Ala Glu Thr Met Tyr Asp

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124          70          75          80
126 AAA ATA CTA AAA AAT CTG TCT CGA AGT AGA AGG CTA ACA AGT GAC 588
127 Lys Ile Leu Lys Asn Leu Ser Arg Ser Arg Arg Leu Thr Ser Asp
128          85          90          95
130 AAG GTA GGC CAG GCA TGT TGC AGG CCG GTC GCC TTC GAC GAC GAC 633
131 Lys Val Gly Gln Ala Cys Cys Arg Pro Val Ala Phe Asp Asp Asp
132          100          105          110
134 CTG TCG TTT TTA GAC GAC AGC CTG GTT TAC CAT ATC CTA AGA AAG 678
135 Leu Ser Phe Leu Asp Asp Ser Leu Val Tyr His Ile Leu Arg Lys
136          115          120          125
138 CAT TCC GCT AAA CGG TGT GGA TGT ATC TGA CCTGGCTCC 718
139 His Ser Ala Lys Arg Cys Gly Cys Ile
140          130
142 AGAGACTGCT GTGTATTGCA TTCCTGCTAC ACTGCGAAGA AAGGGACCAA 768
144 GGTTCACAGG AAATATTTGC CCAGAAAGGA AGATAAGGAC CAAGAAGGCA 818
146 GAGGCAGAGG CGGAAGAAGA AGAAGAAAAG AAGGACGAAG GCAGCCATCT 868
148 GTGGGAGCCT GTAGAAGGAG GCCCAGCTAC AG 900
150 (2) INFORMATION FOR SEQ ID NO: 4:
151 (i) SEQUENCE CHARACTERISTICS:
152 (A) LENGTH: 134 amino acid residues
153 (B) TYPE: amino acid
154 (D) TOPOLOGY: linear
155 (ix) FEATURE:
156 (A) NAME/KEY: inferred amino acid sequence for mature
157 rat GDNF
159 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
162 Ser Pro Asp Lys Gln Ala Ala Ala Leu Pro Arg Arg Glu Arg Asn Arg
163 1 5 10 15
165 Gln Ala Ala Ala Ala Ser Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg
166 20 25 30
168 Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu
169 35 40 45
171 Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile
172 50 55 60
174 Phe Arg Tyr Cys Ser Gly Ser Cys Glu Ala Ala Glu Thr Met Tyr Asp
175 65 70 75 80
177 Lys Ile Leu Lys Asn Leu Ser Arg Ser Arg Arg Leu Thr Ser Asp Lys
178 85 90 95
180 Val Gly Gln Ala Cys Cys Arg Pro Val Ala Phe Asp Asp Asp Leu Ser
181 100 105 110
183 Phe Leu Asp Asp Ser Leu Val Tyr His Ile Leu Arg Lys His Ser Ala
184 115 120 125
186 Lys Arg Cys Gly Cys Ile
187 130
189 (2) INFORMATION FOR SEQ ID NO: 5:
190 (i) SEQUENCE CHARACTERISTICS:
191 (A) LENGTH: 562 base pairs
192 (B) TYPE: nucleic acid
193 (C) STRANDEDNESS: single

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194         (D) TOPOLOGY: linear
195     (ix) FEATURE:
196         (A) NAME/KEY: nucleic acid sequence for human GDNF
198     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
202 ATTT TCTCTTTTCT TTTTGAACAG CA AAT ATG CCA GAG GAT TAT CCT      47
203                               Ser Asn Met Pro Glu Asp Tyr Pro
204                               -25                      -20
206 GAT CAG TTC GAT GAT GTC ATG GAT TTT ATT CAA GCC ACC ATT      89
207 Asp Gln Phe Asp Asp Val Met Asp Phe Ile Gln Ala Thr Ile
208                               -15                      -10
210 AAA AGA CTG AAA AGG TCA CCA GAT AAA CAA ATG GCA GTG CTT      131
211 Lys Arg Leu Lys Arg Ser Pro Asp Lys Gln Met Ala Val Leu
212 -5                               1                      5
214 CCT AGA AGA GAG CGG AAT CGG CAG GCT GCA GCT GCC AAC CCA      173
215 Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala Ala Ala Asn Pro
216 10                               15                      20
218 GAG AAT TCC AGA GGA AAA GGT CGG AGA GGC CAG AGG GGC AAA      215
219 Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly Lys
220 25                               30                      35
222 AAC CGG GGT TGT GTC TTA ACT GCA ATA CAT TTA AAT GTC ACT      257
223 Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu Asn Val Thr
224 40                               45                      50
227 GAC TTG GGT CTG GGC TAT GAA ACC AAG GAG GAA CTG ATT TTT      299
228 Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe
229 55                               60                      65
231 AGG TAC TGC AGC GGC TCT TGC GAT GCA GCT GAG ACA ACG TAC      341
232 Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr
233 70                               75
235 GAC AAA ATA TTG AAA AAC TTA TCC AGA AAT AGA AGG CTG GTG      383
236 Asp Lys Ile Leu Lys Asn Leu Ser Arg Asn Arg Arg Leu Val
237 80                               85                      90
239 ACT GAC AAA GTA GGG CAG GCA TGT TGC AGA CCC ATC GCC TTT      425
240 Ser Asp Lys Val Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe
241 95                               100                     105
243 GAT GAT GAC CTG TCG TTT TTA GAT GAT AAC CTG GTT TAC CAT      467
244 Asp Asp Asp Leu Ser Phe Leu Asp Asp Asn Leu Val Tyr His
245 110                              115                     120
247 ATT CTA AGA AAG CAT TCC GCT AAA AGG TGT GGA TGT ATC TGA      509
248 Ile Leu Arg Lys His Ser Ala Lys Arg Cys Gly Cys Ile
249 125                              130
251 CTCCGGCTCC AGAGACTGCT GTGTATTGCA TTCCTGCTAC AGTGCAAAGA      559
253 AAG                                                                562
255 (2) INFORMATION FOR SEQ ID NO: 6:
256     (i) SEQUENCE CHARACTERISTICS:
257         (A) LENGTH: 134 amino acid residues
258         (B) TYPE: amino acid
259         (D) TOPOLOGY: linear
260     (ix) FEATURE:
261         (A) NAME/KEY: inferred amino acid sequence for mature

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262 human GDNF

265 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

267 Ser Pro Asp Lys Gln Met Ala Val Leu Pro Arg Arg Glu Arg Asn Arg
 268 1 5 10 15
 270 Gln Ala Ala Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg
 271 20 25 30
 273 Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu
 274 35 40 45
 276 Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile
 277 50 55 60
 279 Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr Asp
 280 65 70 75 80
 282 Lys Ile Leu Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Ser Asp Lys
 283 85 90 95
 285 Val Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu Ser
 286 100 105 110
 288 Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser Ala
 289 115 120 125
 291 Lys Arg Cys Gly Cys Ile
 292 130

294 (2) INFORMATION FOR SEQ ID NO: 7:

295 (i) SEQUENCE CHARACTERISTICS:

296 (A) LENGTH: 20 base pairs
 297 (B) TYPE: nucleic acid
 298 (C) STRANDEDNESS: single
 299 (D) TOPOLOGY: linear

300 (ix) FEATURE:

301 (A) NAME/KEY: oligonucleotide probe
 302 (D) OTHER INFORMATION: N at positions 3, 15, and 18 is
 303 inosine

304 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

306 CCNGAYAARC ARGCGCNGC 20

308 (2) INFORMATION FOR SEQ ID NO: 8:

309 (i) SEQUENCE CHARACTERISTICS:

310 (A) LENGTH: 223 base pairs
 311 (B) TYPE: nucleic acid
 312 (C) STRANDEDNESS: single
 313 (D) TOPOLOGY: linear

314 (ix) FEATURE:

315 (A) NAME/KEY: nucleic acid sequence for human GDNF

317 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

319 TTCTCTCCCC CACCTCCCGC CTGCCCGCGC A GGT GCC GCC GCC GGA 46
 320 Gly Ala Ala Ala Gly
 321 -5
 323 CGG GAC TTT AAG ATG AAG TTA TGG GAT GTC GTG GCT GTC TGC 88
 324 Arg Asp Phe Lys Met Lys Leu Trp Asp Val Val Ala Val Cys
 325 1 5 10
 327 CTG GTG CTG CTC CAC ACC GCG TCC GCC TTC CCG CTG CCC GCC 130
 328 Leu Val Leu Leu His Thr Ala Ser Ala Phe Pro Leu Pro Ala

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/991,119

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TIME: 16:40:58

Input Set : N:\Crif3\RULE60\09991119.raw

Output Set: N:\CRF3\01282002\I991119.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:46 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:56 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
L:60 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=2
L:63 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:566 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:569 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:572 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:575 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:578 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:581 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:583 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:587 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:591 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:595 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:599 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:603 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:607 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:611 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:615 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:619 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:623 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25